RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10/569,010
Source:	IFWO
Date Processed by STIC:	05/31/2006
•	

ENTERED



IFWO

RAW SEQUENCE LISTING DATE: 05/31/2006
PATENT APPLICATION: US/10/596,010 TIME: 10:44:24

```
3 <110> APPLICANT: University of Copenhagen
       Andreasson, Erik
 5
        Brodersen, Peter
 6
        Jenkins, Tom
 7
        Mundy, John
8
         Petersen, Nikolaj
9
        Thorgrimsen, Stefan
         Rocher, Anne
10
12 <120> TITLE OF INVENTION: PLANT DISEASE RESISTANCE AND SAR REGULATOR PROTEIN
14 <130> FILE REFERENCE: 09663.00690SWO
16 <140> CURRENT APPLICATION NUMBER: 10/596,010
17 <141> CURRENT FILING DATE: 2006-05-25
19 <150> PRIOR APPLICATION NUMBER: PCT/DK2004/000822
20 <151> PRIOR FILING DATE: 2004-11-26
22 <150> PRIOR APPLICATION NUMBER: DK PA200301759
23 <151> PRIOR FILING DATE: 2003-11-28
25 <150> PRIOR APPLICATION NUMBER: US 60/526,319
26 <151> PRIOR FILING DATE: 2003-12-01
28 <160> NUMBER OF SEQ ID NOS: 28
30 <170> SOFTWARE: PatentIn version 3.3
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 669
34 <212> TYPE: DNA
35 <213> ORGANISM: Arabidopsis sp.
37 <400> SEQUENCE: 1
38 atggatccgt cggagtattt tgccggcggc aatccttccg atcaacagaa ccagaagcgg
                                                                          60
40 cagetteaga tetgtggtee tegteettea eetettagtg tteacaaaga eteteacaaa
                                                                         120
42 atcaagaaac ctccaaaaca ccctgcgccg ccgccaaatc gtgaccaacc gccgccgtat
                                                                         180
44 attectagag ageeggtggt tatetaegee gtateeeca aggttgtaea egeaacegeg
                                                                         240
46 totgagttca tgaacgtagt ccagcgactc acagggatct cctctggtgt tttcctcgaa
                                                                         300
48 tctggcggcg gtggagatgt ttcaccggcg gcgaggctag cgtccacgga aaatgctagt
                                                                         360
                                                                         420
50 ccaagaggag gaaaagaacc ggctgcgaga gatgagacgg tggaaatcaa cacggctatg
52 gaagaagcag ctgaatttgg tggttatgct ccgggaatac tctcgccatc tccggccttg
                                                                         480
54 ttgccaacag cttctaccgg gatattctct ccgatgtatc atcaaggtgg gatgttttcg
                                                                         600
56 coggetatac cactgggatt attetegeeg gegggattta tgageeegtt tegaagteet
58 ggctttacta gtttggtagc ttcaccaact tttgctgatt tctttagtca tatttgggat
                                                                         660
                                                                         669
60 caagattag
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 222
65 <212> TYPE: PRT
66 <213> ORGANISM: Arabidopsis sp.
68 <400> SEQUENCE: 2
70 Met Asp Pro Ser Glu Tyr Phe Ala Gly Gly Asn Pro Ser Asp Gln Gln
```

71 1 5 10 15	
74 Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu	
75 20 25 30	
78 Ser Val His Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro	
79 35 40 45	
82 Ala Pro Pro Pro Asn Arg Asp Gln Pro Pro Pro Tyr Ile Pro Arg Glu	
83 50 55 60	
86 Pro Val Val Tie Tyr Ala Val Ser Pro Lys Val Val His Ala Thr Ala	•
87 65 70 75 80	
90 Ser Glu Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser Gly	
91 85 90 95	
94 Val Phe Leu Glu Ser Gly Gly Gly Asp Val Ser Pro Ala Ala Arg	
95 100 105 110	
98 Leu Ala Ser Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro Ala	
99 115 120 125	
102 Ala Arg Asp Glu Thr Val Glu Ile Asn Thr Ala Met Glu Glu Ala Ala	
103 130 135 140	
106 Glu Phe Gly Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser Pro Ala Leu	
107 145 150 150 155 155 160	
110 Leu Pro Thr Ala Ser Thr Gly Ile Phe Ser Pro Met Tyr His Gln Gly	
111 165 170 175	
114 Gly Met Phe Ser Pro Ala Ile Pro Leu Gly Leu Phe Ser Pro Ala Gly	
115 180 185 190	
118 Phe Met Ser Pro Phe Arg Ser Pro Gly Phe Thr Ser Leu Val Ala Ser	
119 195 200 205	
122 Pro Thr Phe Ala Asp Phe Phe Ser His Ile Trp Asp Gln Asp	
123 210 215 220	
126 <210> SEQ ID NO: 3	
127 <211> LENGTH: 16	
128 <212> TYPE: DNA	
129 <213> ORGANISM: Arabidopsis sp.	
131 <400> SEQUENCE: 3	1.0
132 atggatccgt cggagt	16
135 <210> SEQ ID NO: 4	
136 <211> LENGTH: 16	
137 <212> TYPE: DNA	
138 <213> ORGANISM: Arabidopsis sp. 140 <400> SEQUENCE: 4	
141 ctaatcttca tcccaa	16
144 <210> SEO ID NO: 5	
145 <211> LENGTH: 720	
146 <212> TYPE: DNA	
147 <213> ORGANISM: Arabidopsis sp.	
147 (213) OKGANISM: ATABITOOPSIS SP. 149 (400) SEQUENCE: 5	
150 atggataata gatcgccaag atcaagagga atcttgggtc cgagaccaat accattgaaa	60
152 gtccgtggag attcgcacaa gatcatcaag aagccaccac tagcgccgcc acacccgcaa	120
152 geocgegag decogeded gardareday dayeedeede edgegeege dedocegeda 154 ccacaaccac cacaaaccca tcagcaagaa ccgtcacaat cgcggccgcc acctggtccc	180
156 gtgattatat acacagtate teccaggatt atecatacae accetaataa etteatgaca	
	240
158 ttgqtccaac gtctcacagg taaaacctcc acctccacaa catcctcctc ctattcttca	240 300

```
160 tctacgtcag caccaaaaga cgcgtcaaca atggttgata catctcatgg gttgatatct
    162 ccggcggctc ggtttgctgt tacagagaag gctaatatct caaacgaact agggacattt
                                                                               420
    164 gttggaggcg aagggactat ggatcaatat tatcattatc atcatcatca tcatcatcaa
                                                                               480
    166 gaacaacaac atcaaaatca agggttcgag cggccaagtt tccaccatgc tgggatttta
                                                                               540
    168 tegeegggae etaattetet geegteggta teaceggaet tetttteeae tattggaeca
                                                                               600
    170 accgatecae aaggttttte gtegttettt aatgaettta aetetateet teagagtagt
                                                                               660
    172 ccatcgaaga ttcagtctcc ttcttctatg gaccttttca acaatttctt tgattcttga
                                                                               720
    175 <210> SEQ ID NO: 6
    176 <211> LENGTH: 239
    177 <212> TYPE: PRT
    178 <213> ORGANISM: Arabidopsis sp.
    180 <400> SEQUENCE: 6
    182 Met Asp Asn Arg Ser Pro Arg Ser Arg Gly Ile Leu Gly Pro Arg Pro
                                             10
    186 Ile Pro Leu Lys Val Arg Gly Asp Ser His Lys Ile Ile Lys Lys Pro
    187
                     20
     190 Pro Leu Ala Pro Pro His Pro Gln Pro Gln Pro Pro Gln Thr His Gln
    191
                 35
                                     40
though 194. Glu Glu Pro Ser Gln Ser Arg Pro Pro Pro Gly Pro Val Ile Ile Tyr.
                                                                              - 100 m
            50
                                 55 · ·
                                                      6 Ü
    198 Thr Val Ser Pro Arq Ile Ile His Thr His Pro Asn Asn Phe Met Thr
                             70
                                                  75
    202 Leu Val Gln Arg Leu Thr Gly Lys Thr Ser Thr Ser Thr Thr Ser Ser
                         85
                                             90
    206 Ser Tyr Ser Ser Ser Thr Ser Ala Pro Lys Asp Ala Ser Thr Met Val
    207
                     100
                                         105
                                                              110
    210 Asp Thr Ser His Gly Leu Ile Ser Pro Ala Ala Arg Phe Ala Val Thr
                                     120
    214 Glu Lys Ala Asn Ile Ser Asn Glu Leu Gly Thr Phe Val Gly Glu Glu
                                 135
    218 Gly Thr Met Asp Gln Tyr Tyr His Tyr His His His His His Gln
    222 Glu Gln Gln His Gln Asn Gln Gly Phe Glu Arg Pro Ser Phe His His
    223
                         165
                                              170
    226 Ala Gly Ile Leu Ser Pro Gly Pro Asn Ser Leu Pro Ser Val Ser Pro
    227
                     180
                                         185
    230 Asp Phe Phe Ser Thr Ile Gly Pro Thr Asp Pro Gln Gly Phe Ser Ser
                 195
                                     200
                                                          205
    234 Phe Phe Asn Asp Phe Asn Ser Ile Leu Gln Ser Ser Pro Ser Lys Ile
             210
                                 215
    238 Gln Ser Pro Ser Ser Met Asp Leu Phe Asn Asn Phe Phe Asp Ser
    239 225
                             230
                                                  235
    242 <210> SEQ ID NO: 7
     243 <211> LENGTH: 20
     244 <212> TYPE: DNA
     245 <213> ORGANISM: Arabidopsis sp.
     247 <400> SEQUENCE: 7
    248 atggataata gatcgccaag
                                                                                 20
    251 <210> SEQ ID NO: 8
```

```
252 <211> LENGTH: 21
      253 <212> TYPE: DNA
      254 <213> ORGANISM: Arabidopsis sp.
      256 <400> SEQUENCE: 8
                                                                                                                                                         21
      257 tcaagaatca aagaaattgt t
      260 <210> SEQ ID NO: 9
                                                                                            The second secon
    .261 <211> LENGTH: 791
      262 <212> TYPE: DNA
      263 <213> ORGANISM: Brassica oleracea
      265 <400> SEQUENCE: 9
      266 taatttttcc ctttttttt tgtttataaa tgttttggtc aatactagct cgtcgtcgac
                                                                                                                                                        60
      268 aaagattcat ttcgattccc aaaccacaca agaagaacac aaattagctc gaaagaaaca
                                                                                                                                                       120
      270 aactettttg agaaaataat ggateegteg gagtettteg eeggeggeaa teetteegae
                                                                                                                                                       180
      272 caacagaacc agaaacgtca gcttcagatc tgtggtcctc gtccctcacc tctcagcgtc
      274 aacaaagact ctcacaagat caagaaacct cctaaacacc ctgctcctcc gcctcagcat
                                                                                                                                                       300
      276 egegaceaag eteegeteta egetgetega gageeggtgg teatetaege egtetegeeg
                                                                                                                                                       360
      278 aaagtcgtcc acaccacagc ctcggatttc atgaacgtcg tccagcgtct caccggcatc
                                                                                                                                                       420
      280 teatecgeeg tetteetega ateeggtaac ggeggagatg tateteegge ggegagaete
                                                                                                                                                       480
್ರಾಸ್ತ282 geogogacog agaatgoaag. coogagagga ggaaaagaac ಅಂಥtgatgge ggetaaagat .... 540 , 👵
   284 gagacggtgg aaatcgcgac ggctatggaa gaagcagccg agttgagcgg ctatgcgccg
                                                                                                                                                       600
      286 gggatactet eccettetee ggetatgtta eegacagett etgeeggaat attetegeag
                                                                                                                                                       660
      288 atgactactc accaaggtgg gatgttctcg ccgggattgt tttcgccggc ggggttaatg
                                                                                                                                                       720
      290 ageocgtttg gttttgctag ettggttgct tetecaaegt ttgetgattt gttcagtcat
                                                                                                                                                       780
      292 atttggggat a
                                                                                                                                                       791
      295 <210> SEQ ID NO: 10
      296 <211> LENGTH: 217
      297 <212> TYPE: PRT
      298 <213> ORGANISM: Brassica oleracea
      300 <400> SEQUENCE: 10
      302 Met Asp Pro Ser Glu Ser Phe Ala Gly Gly Asn Pro Ser Asp Gln Gln
      303 1
                                                                                     10
       306 Asn Gln Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu
      307
                                     20
                                                                              25
      310 Ser Val Asn Lys Asp Ser His Lys Ile Lys Lys Pro Pro Lys His Pro
                              35
                                                                     40
      314 Ala Pro Pro Pro Gln His Arg Asp Gln Ala Pro Leu Tyr Ala Ala Arg
                                                              55
      318 Glu Pro Val Val Ile Tyr Ala Val Ser Pro Lys Val Val His Thr Thr
      319 65
                                                      70
                                                                                             75
      322 Ala Ser Asp Phe Met Asn Val Val Gln Arg Leu Thr Gly Ile Ser Ser
                                              85
                                                                                      90
      326 Ala Val Phe Leu Glu Ser Gly Asn Gly Gly Asp Val Ser Pro Ala Ala
                                                                             105
      330 Arg Leu Ala Ala Thr Glu Asn Ala Ser Pro Arg Gly Gly Lys Glu Pro
                              115
                                                                     120
                                                                                                             125
      334 Val Met Ala Ala Lys Asp Glu Thr Val Glu Ile Ala Thr Ala Met Glu
                                                              135
       338 Glu Ala Ala Glu Leu Ser Gly Tyr Ala Pro Gly Ile Leu Ser Pro Ser
       339 145
                                                      150
                                                                                              155
```

```
342 Pro Ala Met Leu Pro Thr Ala Ser Ala Gly Ile Phe Ser Gln Met Thr
                                          170
   343
                       165
   346 Thr His Gln Gly Gly Met Phe Ser Pro Gly Leu Phe Ser Pro Ala Gly
   347
                  180
                                      185
   350 Leu Met Ser Pro Phe Gly Phe Ala Ser Leu Val Ala Ser Pro Thr Phe
        ∾ 195
                                  200
   354 Ala Asp Leu Phe Ser His Ile Trp Gly
- 1 - 355
         210
   358 <210> SEQ ID NO: 11
   359 <211> LENGTH: 20
   360 <212> TYPE: DNA
   361 <213> ORGANISM: Brassica oleracea
   363 <400> SEQUENCE: 11
   364 atggatccgt cggagtcttt
                                                                             20
   367 <210> SEO ID NO: 12
   368 <211> LENGTH: 20
   369 <212> TYPE: DNA
   370 <213> ORGANISM: Brassica oleracea
  372 <400> SEQUENCE: 12
                                                                         ~ 20".-
   373 tatccccaaa tatgactgaa
   376 <210> SEQ ID NO: 13
   377 <211> LENGTH: 878
   378 <212> TYPE: DNA
   379 <213> ORGANISM: Brassica oleracea
   381 <400> SEQUENCE: 13
   382 aaaagtcaac attttgaaag tcaaactaat cggtctcaga aaacaaaaat aactttgtgt
   384 gttgatgttt aggtcaatat actcgtcgtc aaaacatccc ttcaatttct cagaccaaac
                                                                            120
   386 acagagaaga aacaagttgg atccaaactc tctacaacaa aaagtagtga acgagagaag
                                                                            180
   388 ctctccccaa gcgtttaatg gatccgtcgg agcacttcgc cggcggtaat cctttcgatc
                                                                            240
   390 aacagactec aaaacgteag etteagatet gtggeeeteg teetteacet etaagegtea
   392 acaaagactc tcacaagatc aagaaacctc ccaggcaccc tgctccacct cctcagcatc
                                                                            360
   394 accgcgacca agetecgete taccetecte gagageeggt ggttatetae geegtetege
                                                                            420
   396 cgaaagtcgt gcacaccaca acctccgatt tcatgaacgt cgtccagcgt ctcaccggga
                                                                            480
   398 teteeteega ggtetteete gaateaagaa acgaeggaga tgtateaceg geggegagae
                                                                            540
                                                                            600
   400 tegeegegae ggagaatget ageeegagag gaggaaagga aceggtggaa agetegaegg
   402 ctatggaaga agcagctgag ttcggttgtt atgtgccggg aatactctcg ccgtctccgg
                                                                            660
   404 ctatgttacc gaccgttccc gccggaattt tctctccgat gtttcaccta ggtgggttgt
                                                                            720
   406 tttcgccggc gttgccgccg ggattatttt cgccggcagg attaatgagc cctggttatg
                                                                            780
   408 ctagtttggc gtcaccaaat tttgctgatt tcttcagtca catttgggat ccttagagaa
                                                                            840
   410 tagattatta gtttttttta ttatttacat tttatgta
                                                                            878
   413 <210> SEQ ID NO: 14
   414 <211> LENGTH: 212
   415 <212> TYPE: PRT
   416 <213> ORGANISM: Brassica oleracea
   418 <400> SEQUENCE: 14
   420 Met Asp Pro Ser Glu His Phe Ala Gly Gly Asn Pro Phe Asp Gln Gln
   421 1
                      5
                                           10
   424 Thr Pro Lys Arg Gln Leu Gln Ile Cys Gly Pro Arg Pro Ser Pro Leu
   425
                                       25
```

VERIFICATION SUMMARY

. . . .

DATE: 05/31/2006

PATENT APPLICATION: US/10/596,010

TIME: 10:44:25